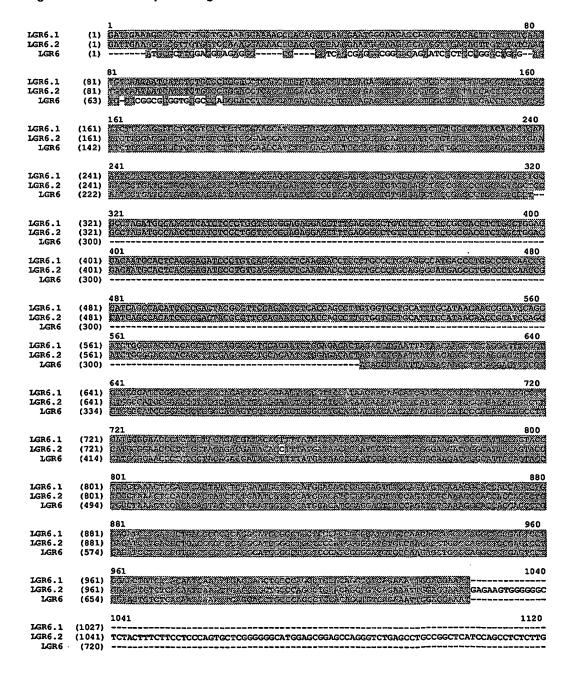
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Figure 1 Nucleotide sequence alignment of LGR6.1 and LGR6.2 and LGR6.



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Figure 1 (cont.)

LGR6.1 LGR6.2 LGR6	(1027) (1121) (720)	CTGCCCTACCCCCCCCCCAAAAAAAAAAAAAAAAAAAAA
LGR6.1 LGR6.2 LGR6	(1098) (1201) (791)	1201 1200 CONTROL OF THE CONTROL OF
6.1 6.2 GR6	(1178) (1281) (871)	1281 1360 FACT AND DECEMBER OF THE PERSON OF SECURITY SECURITY OF THE PERSON OF THE P
6.1 6.2 GR6	(1258) (1361) (951)	1361 1440 CTCS RESCRIPTION OF THE CONTROL OF THE CO
6.1 6.2 GR6	(1338) (1441) (1031)	
6.1 6.2 GR6	(1418) (1521) (1111)	1521 1600 CCCCC PSGC I CCTF CAGGA AGCARGATE PLANTAGES AT COMPANY TO BE TRUE AS CAGGA AGGCCCT CGCC PSGC AGCARGA AGCAR
6.1 6.2 GR6	(1498) (1601) (1191)	Propagation of the Arter and Transfer and Control and
6.1 6.2 GR6	(1578) (1681) (1271)	1681 1760 SERVICES TO SERVICE CONTROL OF THE
6.1 6.2 GR6	(1658) (1761) (1351)	1761 1840 ESCURPTION OF THE CONTROL
6.1 6.2 GR6	(1738) (1841) (1431)	1841 1920 FORTON OF CAST CONTROL OF A PROPERTY OF A CONTROL OF A CONT
6.1 6.2 GR6	(1818) (1921) (1511)	1921 2000 GGGCALTGGGTACTACTACTACTACTACTACTACTACTACTACTACTACT
6.1 6.2 GR6	(1898) (2001) (1591)	2001 2080 PURPLE CONTROL OF THE CONT
6.1 6.2 GR6	(1978) (2081) (1671)	CONTROL TO A PROCESSING THE RESERVE CONTROL OF THE
6.1 6.2 3R6	(2058) (2161) (1751)	

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Figure 1 (cont.)

LGR6.1 LGR6.2 LGR6	(2138) (2241) (1831)	232 CONDENSE AND CONTROL OF THE CONT	0
LGR6.1 LGR6.2 LGR6	(2218) (2321) (1911)	2321 240 OUGS CONTROL CAN SECURITY OF STANCE OF A LITTURE OF THE CONTROL OF THE	10
16.1 16.2 1GR6	(2298) (2401) (1991)	Holdet Corrective and the control of	10
16.1 16.2 IGR6	(2378) (2481) (2071)	256 TTGLACCLOSTALTTEGGG-MUSACCTTOGGC-SETTEGGC-CCCCG-AMBRICACTC M-SIGTEGGT-CCTATAGE CCC MTGLACCLCCACCTCCGC-SARCACCTTOGGC-CCCCGC-AMBRICACTC M-SIGTEGGT-CCCCTATAGE CCCC MTGLACCLCCACCTCCGC-SARCACCTTOGGC-CCCCCACCTCGC-CCCCCCCCCCCCCCCCCCCCCCC	
:6.1 :6.2 :GR6	(2458) (2561) (2151)	2561 2669 GEOGRAPHICA CONTRACTOR AND	
:6.1 :6.2 :GR6	(2538) (2641) (2231)	272 PERMICTAGES PE	
.6.1 .6.2 GR6	(2618) (2721) (2311)	2721 CAGGETOSALESSASSELT STEEMASCENERGESSALT DETTRICEDATE SALES AGENTOSALESSAS DE CONTRESENTATION DE LA RECONTRES DE LA RECON	
.6.1 .6.2 GR6	(2698) (2801) (2391)	2801 CCTOPT GARSCUTCH SHOPT COLOR SECRETARION ACCIDENTATE OF CONTRACTORS STORE STOR	
.6.1 .6.2 GR6	(2778) (2881) (2471)	2981 2981 FULL TRANSPORT CONTROL OF ARTICLE FOR TOO CONTROL C	
6.1 6.2 GR6	(2858) (2961) (2485)	2961 304 ESCTGCTTCTANAGNANTACAGCANARCTCNSTAGTCTGNTCTATAGCAGGATGGCCAGTACCCTGGCTCAGTGA ESCTGCTTCTANAGNANTACAGCGAAACTCAGGGTGGGTGGTGAGTAGCAGGATGGCCGAGTACTGACTG	are.
6.1 6.2 GR6	(2938) (3041) (2485)	3041 ACOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOT	
6.1 6.2 GR6	(3018) (3121) (2485)	3121 GEODETETTCOTTGTCAPGTCTGAAGCTCTGGACCACCACCACCACCACCACCACCACCACCACCACCAC	
6.1 6.2 3R6	(3098) (3201) (2485)	3201 32 GRENGTORAGIGGTTGATEAGGGACAGTGGACAGGACAGCTGACAGAAAAGGGCTGAAGAGATTTC GACAGTGAAGGGGTTGATCAGGGGACAGTGGACAGGAGAGACCTCAGAGAAAAGGCCTGAAGAGATTTC GACAGTGAAGGGTTGATCAGGGGACAGTGGACAGGGAGAGACCTCAGAGAAAAGGCCTGAAAAAGACAGAAAAG	
6.1 6.2 3R6	(3178) (3281) (2485)	3281 GRIGAGTERTGGRITAGGATAGRAMTGGETTEEATGFREERTHAATCTTGREATATATGCRITAGAACATTEETA ETGTGACTCATGGATAGGATAGAAATGGGTCCCATGGACATTAATCTTGACATATGCATATGCATAAAGACTTGCTA	T

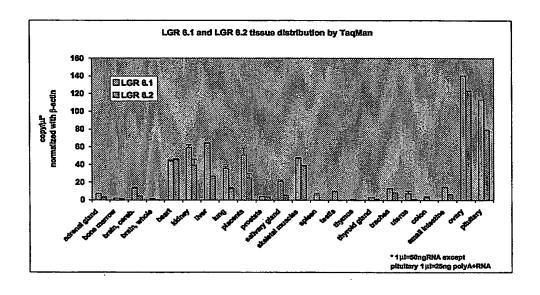
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Figure 1 (cont.)

LGR6.1 LGR6.2 LGR6	(3258) (3361) (2485)	3361 3440 BARTARS FITGA MAGATTA CAMARARARARARARARARARARARARARARARARARARA
		3441 3451
LGR6.1	(3307)	
LGR6.2	(3441)	AAAAAAAAA
GR6	(2485)	

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Figure 2



~	ıra	•

GR6	MRLEGEGRSARAGONLSRAGSARRGAPRDLSMNNLTELQPGLFHHLRFLEELRLSGNHLS
GR6.1	
LGR6.2	MGRPRLTLVCQ -VSIIISAR DLSMNNLTELQPGLFHHLRFLEELRLSGNHLS
. 2. UGRO	MGRPRLTLVCQ-VSIIISARDLSMNNLTELQPGLFHHLRFLE ELRLSGNHLS *. *: . *:* *** ***********************
LGR6	HIPGQAFSGLYSLKILMLQNNQLGGIPAEALWELPSLQSL
LGR6.1	hipgqafsglyslkilmlqnnqlggifaealwelpslqslrldanlislvpersfeglss
.cR6.2	hipgqafsglyslkilmlqnnqlggipaealwelpslqslrldanlislvpersfeglss

₹6	
₹6.1	LRHIWLDDNALTEIPVRALNN LPALQAMTLALNRISHIPDYAFONLTSLVVLHLHNNRIO
₹6.2	
10.2	LRHLWLDDNALTEIPVRALNNLPALQAMTLALNRISHIPDYAFQNLTSLVVLHLHNNRIQ
₹6	DI MANYI AMBRIA TRIII ARI ARI ARIBANI TUR TRIVIS TAMBAN T
	DLNYNKLQEFPVAIRTLGRLQELGFHNNN IKAIPEKAFMGNPLL
₹6.1	Higthsfeglhnletldlnynkloefpvairtigrloeigfhnnnikaipekafmgnpll
₹6.2	HLGTHSFEGLHNLETLDLNYNKLQEFPVAIRTLGRLQELGFHNNNIKAIPEKAFMGNPLL ***********************************
16	QTIHFYDNPIQFVGRSAFQYLPKLHTLSLNGAMDIQEFPDLKGTTSLEILTLTRAGIRLL
₹6.1	QT1HFYDNP1QFVGRSAFQYLPKLHTLSLNGAMD1QEFPDLKGTTSLE1LTLTRAG1RLL
₹6.2	QTIHLYDNPIQFVGRSAFQYLPKLHTLSLNGAMDIQEFPDLKGTTSLEILTLTRAGIRLL

16 ΄	PSGMCQQLPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLSSLQAL
₹6.1	PSGMCQQLPRLRVLELSHNQIEELPSLHRCQKLEEIGLQHNRIWEIGADTFSQLSSLQAL
16.2	PSGMCQQLPRLRVLELSHNQIEELPSLHRCQKLEEMRS
(0.2	**************************************
	DI (1701) TRATITATI PART (1701) TRATICATION DE RESIDENCE
16	DLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKLKGNLALSQAFSKD
16.1	DLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKLKGNLALSQAFSKD
16.2	*** .*
t6	SFPKLRILEVP XXXXCCPYGMCASFFKASGQWEAEDLHLDDEESSKRPLGLLARQAENHY
t6.1	SFPKLRILEVP YAYOCCPYGMCASFFKASGQWEAEDLHLDDEESSKRPLGLLARQAENHY
t6.2	ARGAWSGARV
	* * * :
:6	DQDLDELQLEMEDSKPHPSVQCSPTP GPFKPCEYLFESWGIRLAVWAIVLLSVLCNGLVL
16.1	DQDLDELQLEMEDSKPHPSVQCSPTP GPFKECEYLFESWGIRLAVWAIVLLSVLCNGLVL
16.2	
:6	LTVFAGGPVPLPPVKFVVGAIAGANTLTGISCGLLASVDALTFGOFSEYGARWETGLGCR
ા6.1	LTVFAGGPVPLPPVKFVVGAIAGANTLTGISCGLLASVDALTFGOFSEYGARWETGLGCR
:6.2	
:6	ATGFLAVLGSEASVLILTLAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLAAAL
:6.1	atgflavlgseasvilittaavocsvsvscvraygkspsigsvragvigclalagiaaal
:6.2	***************************************
:6	PLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMMNSFCFLVVAGAYIKLYCDLP
:6.1	PLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMMNSFCFLVVAGAYIKLYCDLP
:6.2	WEALTH CONTRACTOR OF THE PROPERTY OF THE PROPE
.6	EAVWDCAMVRHVAWLIFADGLLYCFVAFLSFASMLGLFPVTPEAVKSVLLVVLPLPACLN
.6.1	EAV WDCAMVRHVAWLIFADGLLYCPVAFLSFASMLGLFPVTPEAVKSVLLVVLPLPACLN
.6.2	

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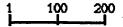
Figure 3 (cont.)

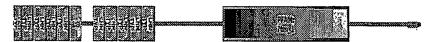
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LGR6.1	PLLYLLFNPHFRDDLRRLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLILEAS
LGR6.2	
LGR6	EAGRPPGLETYGFPSVTLISCOOPGAPRLEGSHCVEPEGNHFGNPOPSMDGELLLRAEGS
LGR6.1	EAGRPPGLETYGFPSVTLISCOOPGAPRLEGSHCVEPEGNHFGNPOPSMDGELLLRAEGS
LGR6.2	
36	TPAGGGLSGGGGFOPSGLALLHTY
36.1	TPAGGGLSGGGFOPSGLAFASHV
36.2	

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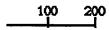
Figure 4.

Domains within the query sequence LGR6 of 828 residues



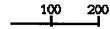


mains within the query sequence LGR6.1 of 915 residues





mains within the query sequence LGR6.2 of 348 residues





Insmembrane segments as predicted by the <u>TMHMM2</u> program (), coiled coil regions determined by <u>Coils2</u> program () and Segments of low compositional complexity, determined by the <u>SEG</u> program (), signal peptides determined by the <u>Sigcleave</u> program (), GPI anchors are indicated by (), gions containing repeats detected by <u>Prospero</u>, but not covered by domains are indicated by ().